

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/468,011A

1812

#11
Q2
924-97DATE: 09/16/97
TIME: 10:08:59

INPUT SET: S20361.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1

2

3 (1) General Information:

4

5 (i) APPLICANT: Soppet, Daniel R
6 Yi, Li
7 Rosen, Craig A
8 Ruben, Steven9
10 (ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
11 HLTDG74

12

13 (iii) NUMBER OF SEQUENCES: 28

14

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
17 Stewart & Olstein
18 (B) STREET: 6 Becker Farm Road
19 (C) CITY: Roseland
20 (D) STATE: NJ
21 (E) COUNTRY: USA
22 (F) ZIP: 07068-1739

23

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: 3.5 INCH DISKETTE
26 (B) COMPUTER: IBM PS/2
27 (C) OPERATING SYSTEM: MS-DOS
28 (D) SOFTWARE: WORD PERFECT 5.1

29

30 (vi) CURRENT APPLICATION DATA:

31 (A) APPLICATION NUMBER: 08/468,011
32 (B) FILING DATE: 06-JUN-1995
33 (C) CLASSIFICATION:

34

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: MULLINS, J.G.
37 (B) REGISTRATION NUMBER: 33,073
38 (C) REFERENCE/DOCKET NUMBER: 325800-458 (PF201)

39

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 201-994-1700
42 (B) TELEFAX: 201-994-1744

43

44 (2) INFORMATION FOR SEQ ID NO:1:

45

INPUT SET: S20361.raw

47 (i) SEQUENCE CHARACTERISTICS:
 48 (A) LENGTH: 2003 base pairs
 49 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: single
 51 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: cDNA

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

57 GTTTGCTCTG	GGCAGCCAAG	TTGGCATATT	CGAAGCTTTT	TCCGGGCTCT	GGAGGAGGGT	60
58	CCCTGCTTCT	TCCTACAGCC	GTTCCGGGC	ATG GCC TGG CTG GGG GCG TCG CTC	Met Ala Trp Leu Gly Ala Ser Leu	113
60	1	5				
62	CAC GTC TGG GGT TGG CTA ATG CTC GGC AGC TGC CTC CTG GCC AGA GCC	His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala	161			
64	10	15	20			
66	CAG CTG GAT TCT GAT GGC ACC ATC ACT ATA GAG GAG CAG ATT GTC CTT	Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu	209			
68	25	30	35	40		
70	GTG CTG AAA GCG AAA GTA CAA TGT GAA CTC AAC ATC ACA GCT CAA CTC	Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu	257			
72	45	50	55			
74	CAG GAG GGA GAA GGT AAT TGT TTC CCT GAA TGG GAT GGA CTC ATT TGT	Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys	305			
76	60	65	70			
78	TGG CCC AGA GGA ACA GTG GGG AAA ATA TCG GCT GTT CCA TGC CCT CCT	Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro	353			
80	75	80	85			
82	TAT ATT TAT GAC TTC AAC CAT AAA GGA GTT GCT TTC CGA CAC TGT AAC	Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn	401			
84	90	95	100			
86	CCC AAT GGA ACA TGG GAT TTT ATG CAC AGC TTA AAT AAA ACA TGG GCC	Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala	449			
88	105	110	115	120		
90	AAT TAT TCA GAC TGC CTT CGC TTT CTG CAG CCA GAT ATC AGC ATA GGA	Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly	497			
92	125	130	135			
94	AAG CAA GAA TTC TGT GAA CGC CTC TAT GTA ATG TAT ACC GTT GGC TAG	Lys Gln Glu Phe Cys Glu Arg Leu Tyr Val Met Tyr Thr Val Gly Tyr	545			
96	140	145	150			
98	TCC ATC TCT TTT GGT TCC TTG GCT GTG GCT ATT CTC ATC ATT GGT TAC		593			

RAW SEQUENCE LISTING
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100	Ser Ile Ser Phe Gly Ser Leu Ala Val Ala Ile Leu Ile Ile Gly Tyr			
101	155	160	165	
102				
103	TTC AGA CGA TTG CAT TGC ACT AGG AAC TAT ATC CAC ATG CAC TTA TTT		641	
104	Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe			
105	170	175	180	
106				
107	GTC TCT TTC ATG CTG AGA GCT ACA AGC ATC TTT GTC AAA GAC AGA GTA		689	
108	Val Ser Phe Met Leu Arg Ala Thr Ser Ile Phe Val Lys Asp Arg Val			
109	185	190	195	200
110				
111	GTC CAT GCT CAC ATA GGA GTA AAG GAG CTG GAG TCC CTA ATA ATG CAG		737	
112	Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln			
113	205	210	215	
114				
115	GAT GAC CCA CAA AAT TCC ATT GAG GCA ACT TCT GTG GAC AAA TCA CAA		785	
116	Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr Ser Val Asp Lys Ser Gln			
117	220	225	230	
118				
119	TAT ATC GGG TGC AAG ATT GCT GTT GTG ATG TTT ATT TAC TTC CTG GCT		833	
120	Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala			
121	235	240	245	
122				
123	ACA AAT TAT TAT TGG ATC CTG GTG GAA GGT CTC TAC CTG CAT AAT CTC		881	
124	Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu			
125	250	255	260	
126				
127	ATC TTT GTG GCT TTC TTT TCG GAC ACC AAA TAC CTG TGG GGC TTC ATC		929	
128	Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile			
129	265	270	275	280
130				
131	TTG ATA GGC TGG GGG TTT CCA GCA GCA TTT GTT GCA GCA TGG GCT GTG		977	
132	Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val			
133	285	290	295	
134				
135	GCA CGA GCA ACT CTG GCT GAT GCG AGG TGC TGG GAA CTT AGT GCT GGA		1025	
136	Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly			
137	300	305	310	
138				
139	GAC ATC AAG TGG ATT TAT CAA GCA CCG ATC TTA GCA GCT ATT GGG CTG		1073	
140	Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu			
141	315	320	325	
142				
143	AAT TTT ATT CTG TTT CTG AAT ACG GTT AGA GTT CTA GCT ACC AAA ATC		1121	
144	Asn Phe Ile Leu Phe Leu Asn Thr Val Arg Val Leu Ala Thr Lys Ile			
145	330	335	340	
146				
147	TGG GAG ACC AAT GCA GTT GGG CAT GAC ACA AGG AAG CAA TAC AGG AAA		1169	
148	Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys			
149	345	350	355	360
150				
151	CTG GCC AAA TCG ACA CTG GTG CTG GTC CTA GTC TTT GGA GTG CAT TAC		1217	
152	Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr			

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153	365	370	375	
154				
155	ATC GTG TTC GTG TGC CTG CCT CAC TCC TTC ACT GGG CTC GGG TGG GAG			1265
156	Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu			
157	380	385	390	
158				
159	ATC CGC ATG CAC TGT GAG CTC TTC AAC TCC TTT CAG GGT TTC TTT			1313
160	Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe			
161	395	400	405	
162				
163	GTG TCT ATC ATC TAC TGC TAC TGC AAT GGA GAG GTT CAG GCA GAG GTG			1361
164	Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val			
165	410	415	420	
166				
167	AAG AAG ATG TGG AGT CGG TGG AAT CTC TCC GTG GAC TGG AAA AGG ACA			1409
168	Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr			
169	425	430	435	440
170				
171	CCG CCA TGT GGC AGC CGC AGA TGC GGC TCA GTG CTC ACC ACC GTG ACG			1457
172	Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr			
173	445	450	455	
174				
175	CAC AGC ACC AGC AGC CAG TCA CAG GTG GCG GCA GCA CAC GCA TGG TGC			1505
176	His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys			
177	460	465	470	
178				
179	TTA TCT CTG GCA AAG CTG CCA AGA TCG CCA GCA GAC AGC CTG ACA GCC			1553
180	Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala			
181	475	480	485	
182				
183	ACA TCA CTT TAC CTG GCT ATG TCT GGA GTA ACT CAG AGC AGG ACT GCC			1601
184	Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala			
185	490	495	500	
186				
187	TCA CAC ACT CTC TCC ACG AGG AGC AAC AAG GAA GAT AGT GGG AGG CAG			1649
188	Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln			
189	505	510	515	520
190				
191	AGA GAT GAT ATT CTA ATG GAG AAG CCT TCC AGG CCT ATG GAA TCT AAC			1697
192	Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn			
193	525	530	535	
194				
195	CCA GAC ACT GAA GGA TGACAAGGAG AAACTGAGGA TGTTCTCTGA ATGGACATGT			1752
196	Pro Asp Thr Glu Gly			
197	540			
198				
199	GTGGCTGACT TTCATGGGC GGTCCAATGG CTGGTTGTGT GAGAGGGCTT GGCTGATACT			1812
200				
201	CCTATGCTTG ACCAAGGAG CTGAAATTC AGTTAAGGTG TTACTTAATA ATAGTTTTA			1872
202				
203	GGCTCCATGA ATTGGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT			1932
204				
205	AGTTTATTAC CTTCTATTGG CATCAAGTTT TCCTCTAAAT TAATGTATGG TATTTGCTCT			1992

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/468,011ADATE: 09/16/97
TIME: 10:09:13

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206
207 GTGATTGTTC A 2003
208
209
210 (2) INFORMATION FOR SEQ ID NO:2:
211
212 (i) SEQUENCE CHARACTERISTICS:
213 (A) LENGTH: 541 amino acids
214 (B) TYPE: amino acid
215 (D) TOPOLOGY: linear
216
217 (ii) MOLECULE TYPE: protein
218
219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
220
221 Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu
222 5 10 15
223
224 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
225 20 25 30
226
227 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
228 35 40 45
229
230 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
231 50 55 60
232
233 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
234 65 70 75 80
235
236 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
237 85 90 95
238
239 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
240 100 105 110
241
242 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
243 115 120 125
244
245 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu
246 130 135 140
247
248 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
249 145 150 155 160
250
251 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg
252 165 170 175
253
254 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr
255 180 185 190
256
257 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys
258 195 200 205

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SEQUENCE VERIFICATION REPORT
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DATE: 09/16/97
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Line

Error

Original Text